D, STEADMAN

RAW SEQUENCE LISTING   DATE: 06/29/2001
PATENT APPLICATION: **US/09/556,178**   TIME: 11:07:40

Input Set : **N:\Crf3\RULE60\09556178.txt**
Output Set: **N:\CRF3\06292001\I556178.raw**

Paper No. 4
DJS 06/29/01

```
        SEQUENCE LISTING
C--> 3 (1) GENERAL INFORMATION:
    5      (i) APPLICANT: Bandman, Olga
    6                    Lal, Preeti
    7                    Guegler, Karl J.
    8                    Shah, Purvi
    9                    Corley, Neil C.
C--> 11    (ii) TITLE OF INVENTION: VESICLE TRAFFICKING PROTEINS
    13   (iii) NUMBER OF SEQUENCES: 9
    15    (iv) CORRESPONDENCE ADDRESS:
    16        (A) ADDRESSEE: Incyte Pharmaceuticals, Inc.
    17        (B) STREET: 3174 Porter Dr.
    18        (C) CITY: Palo Alto
    19        (D) STATE: CA
    20        (E) COUNTRY: USA
    21        (F) ZIP: 94304
    23     (v) COMPUTER READABLE FORM:
    24        (A) MEDIUM TYPE: Diskette
    25        (B) COMPUTER: IBM Compatible
    26        (C) OPERATING SYSTEM: DOS
    27        (D) SOFTWARE: FastSEQ for Windows Version 2.0
    29    (vi) CURRENT APPLICATION DATA:
C--> 30        (A) APPLICATION NUMBER: US/09/556,178
C--> 31        (B) FILING DATE: 20-Apr-2000
    33   (vii) PRIOR APPLICATION DATA:
    34        (A) APPLICATION NUMBER: 08/967,364
    35        (B) FILING DATE:
    37  (viii) ATTORNEY/AGENT INFORMATION:
    38        (A) NAME: Cerrone, Michael C.
    39        (B) REGISTRATION NUMBER: 39,132
    40        (C) REFERENCE/DOCKET NUMBER: PF-0417 US
    42    (ix) TELECOMMUNICATION INFORMATION:
    43        (A) TELEPHONE: 650-855-0555
    44        (B) TELEFAX: 650-845-4166
    47 (2) INFORMATION FOR SEQ ID NO: 1:
    49      (i) SEQUENCE CHARACTERISTICS:
    50        (A) LENGTH: 570 amino acids
    51        (B) TYPE: amino acid
    52        (C) STRANDEDNESS: single
    53        (D) TOPOLOGY: linear
    55    (vii) IMMEDIATE SOURCE:
    56        (A) LIBRARY: THPIPEB01
    57        (B) CLONE: 75871
    62     (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
    64  Met Asn Val Val Phe Ala Val Lys Gln Tyr Ile Ser Lys Met Ile Glu
    65   1               5                  10                  15
    66  Asp Ser Gly Pro Gly Met Lys Val Leu Leu Met Asp Lys Glu Thr Thr
```

ENTERED

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/556,178

DATE: 06/29/2001
TIME: 11:07:41

Input Set : N:\Crf3\RULE60\09556178.txt
Output Set: N:\CRF3\06292001\I556178.raw

```
67                  20                  25                  30
68   Gly Ile Val Ser Met Val Tyr Thr Gln Ser Glu Ile Leu Gln Lys Glu
69           35                  40                  45
70   Val Tyr Leu Phe Glu Arg Ile Asp Ser Gln Asn Arg Glu Ile Met Lys
71       50                  55                  60
72   His Leu Lys Ala Ile Cys Phe Leu Arg Pro Thr Lys Glu Asn Val Asp
73   65                  70     .              75                  80
74   Tyr Ile Ile Gln Glu Leu Arg Arg Pro Lys Tyr Thr Ile Tyr Phe Ile
75                       85                  90                  95
76   Tyr Phe Ser Asn Val Ile Ser Lys Ser Asp Val Lys Ser Leu Ala Glu
77               100                 105                 110
78   Ala Asp Glu Gln Glu Val Val Ala Glu Val Gln Glu Phe Tyr Gly Asp
79           115                 120                 125
80   Tyr Ile Ala Val Asn Pro His Leu Phe Ser Leu Asn Ile Leu Gly Cys
81       130          .        135                 140
82   Cys Gln Gly Arg Asn Trp Asp Pro Ala Gln Leu Ser Arg Thr Thr Gln
83   145               150                 155                 160
84   Gly Leu Thr Ala Leu Leu Leu Ser Leu Lys Lys Cys Pro Met Ile Arg
85       .            165                 170                 175
86   Tyr Gln Leu Ser Ser Glu Ala Ala Lys Arg Leu Ala Glu Cys Val Lys
87               180                 185                 190
88   Gln Val Ile Thr Lys Glu Tyr Glu Leu Phe Glu Phe Arg Arg Thr Glu
89           195                 200                 205
90   Val Pro Pro Leu Leu Leu Ile Leu Asp Arg Cys Asp Asp Ala Ile Thr
91       210                 215                 220
92   Pro Leu Leu Asn Gln Trp Thr Tyr Gln Ala Met Val His Glu Leu Leu
93   225               230                 235                 240
94   Gly Ile Asn Asn Asn Arg Ile Asp Leu Ser Arg Val Pro Gly Ile Ser
95               245                 250                 255
96   Lys Asp Leu Arg Glu Val Val Leu Ser Ala Glu Asn Asp Glu Phe Tyr
97               260                 265                 270
98   Ala Asn Asn Met Tyr Leu Asn Phe Ala Glu Ile Gly Ser Asn Ile Lys
99           275                 280                 285
100  Asn Leu Met Glu Asp Phe Gln Lys Lys Lys Pro Lys Glu Gln Gln Lys
101      290                 295                 300
102  Leu Glu Ser Ile Ala Asp Met Lys Ala Phe Val Glu Asn Tyr Pro Gln
103  305                 310                 315                 320
104  Phe Lys Lys Met Ser Gly Thr Val Ser Lys His Val Thr Val Val Gly
105               325                 330                 335
106  Glu Leu Ser Arg Leu Val Ser Glu Arg Asn Leu Leu Glu Val Ser Glu
107               340                 345                 350
108  Val Glu Gln Glu Leu Ala Cys Gln Asn Asp His Ser Ser Ala Leu Gln
109           355                 360                 365
110  Asn Ile Lys Arg Leu Leu Gln Asn Pro Lys Val Thr Glu Phe Asp Ala
111      370                 375                 380
112  Ala Arg Leu Val Met Leu Tyr Ala Leu His Tyr Glu Arg His Ser Ser
113  385                 390                 395                 400
114  Asn Ser Leu Pro Gly Leu Met Met Asp Leu Arg Asn Lys Gly Val Ser
115               405                 410                 415
```

```
116  Glu Lys Tyr Arg Lys Leu Val Ser Ala Val Val Glu Tyr Gly Gly Lys
117              420             425             430
118  Arg Val Arg Gly Ser Asp Leu Phe Ser Pro Lys Asp Ala Val Ala Ile
119          435             440             445
120  Thr Lys Gln Phe Leu Lys Gly Leu Lys Gly Val Glu Asn Val Tyr Thr
121      450             455             460
122  Gln His Gln Pro Phe Leu His Glu Thr Leu Asp His Leu Ile Lys Gly
123  465             470             475             480
124  Arg Leu Lys Glu Asn Leu Tyr Pro Tyr Leu Gly Pro Ser Thr Leu Arg
125              485             490             495
126  Asp Arg Pro Gln Asp Ile Ile Val Phe Val Ile Gly Gly Ala Thr Tyr
127          500             505             510
128  Glu Glu Ala Leu Thr Val Tyr Asn Leu Asn Arg Thr Thr Pro Gly Val
129          515             520             525
130  Arg Ile Val Leu Gly Gly Thr Thr Val His Asn Thr Lys Ser Phe Leu
131      530             535             540
132  Glu Glu Val Leu Ala Ser Gly Leu His Ser Arg Ser Lys Glu Ser Ser
133  545             550             555             560
134  Gln Val Thr Ser Arg Ser Ala Ser Arg Arg
135              565             570
137  (2) INFORMATION FOR SEQ ID NO: 2:
139       (i) SEQUENCE CHARACTERISTICS:
140            (A) LENGTH: 2342 base pairs
141            (B) TYPE: nucleic acid
142            (C) STRANDEDNESS: single
143            (D) TOPOLOGY: linear
145      (vii) IMMEDIATE SOURCE:
146            (A) LIBRARY: THPIPEB01
147            (B) CLONE: 75871
149      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
151  GGACCTCGCG TCGGGCCAAC AGACTGCGGG GTTAATTTAG CCAGACACGT GGGCGGGAAG      60
152  GGCTGTAGGG TACTTGTCAA TTCGCCGCCA TGAACGTGGT TTTTGCTGTG AAGCAGTACA     120
153  TTTCCAAAAT GATAGAGGAC AGCGGGCCTG GTATGAAAGT ACTTCTCATG GATAAAGAGA     180
154  CGACTGGCAT AGTGAGTATG GTATACACAC AATCGGAGAT TCTACAGAAG GAAGTGTACC     240
155  TCTTTGAACG CATCGATTCT CAAAATCGAG AGATCATGAA ACACCTGAAG GCAATTTGTT     300
156  TTCTTCGACC TACAAAGGAG AATGTGGATT ATATTATTCA GGAGCTCCGA AGACCCAAAT     360
157  ACACTATATA TTTCATTTAT TTCAGTAATG TGATCAGCAA GAGTGACGTG AAGTCATTGG     420
158  CTGAAGCTGA TGAACAGGAA GTTGTGGCTG AGGTTCAGGA ATTTTATGGT GATTACATTG     480
159  CTGTGAACCC ACATTTGTTT TCCCTCAATA TTTTGGGTTG CTGCCAGGGT CGAAATTGGG     540
160  ATCCAGCCCA GCTATCTAGA ACAACTCAAG GGCTTACAGC TCTCCTTTTA TCTCTGAAGA     600
161  AGTGTCCCAT GATTCGTTAT CAGCTCTCAT CAGAGGCAGC AAAGAGACTT GCAGAGTGCG     660
162  TTAAGCAAGT GATAACTAAA GAATATGAAC TGTTTGAATT CCGTCGGACA GAGGTTCCTC     720
163  CATTGCTCCT TATTTTAGAT CGCTGTGATG ATGCCATCAC CCCATTGCTA AACCAGTGGA     780
164  CATATCAGGC CATGGTCCAC GAACTACTAG GCATAAACAA CAATCGGATT GATCTTTCCA     840
165  GAGTGCCGGG AATCAGTAAA GACTTAAGAG AAGTGGTCCT ATCTGCTGAA AATGATGAAT     900
166  TCTATGCTAA TAATATGTAC CTGAACTTTG CTGAGATTGG TAGCAATATA AAGAATCTCA     960
167  TGGAAGATTT TCAGAAGAAG AAACCAAAAG AACAGCAAAA ACTAGAATCA ATAGCAGACA    1020
168  TGAAGGCGTT TGTTGAGAAT TATCCACAGT TCAAGAAAAT GTCTGGGACT GTTTCAAAGC    1080
169  ATGTGACAGT GGTTGGAGAA CTGTCTCGAT TGGTCAGTGA ACGGAATCTG CTGGAGGTTT    1140
```

```
170  CAGAGGTTGA GCAAGAACTG GCCTGTCAAA ATGACCATTC TAGTGCTCTC CAGAATATAA  1200
171  AAAGGCTTCT GCAGAACCCC AAAGTGACAG AGTTTGATGC TGCCCGCCTG GTGATGCTTT  1260
172  ATGCTTTACA TTATGAGCGA CACAGCAGCA ATAGCCTGCC AGGACTAATG ATGGACCTCA  1320
173  GGAATAAAGG TGTTTCTGAG AAGTATCGAA AGCTCGTGTC TGCAGTTGTT GAATATGGTG  1380
174  GTAAACGAGT CAGAGGAAGT GACCTCTTCA GCCCCAAAGA TGCTGTGGCT ATCACCAAAC  1440
175  AATTCCTCAA AGGACTGAAG GGAGTAGAAA ATGTATATAC ACAGCATCAA CCTTTCCTAC  1500
176  ATGAAACCCT GGATCATCTC ATCAAAGGAA GGCTTAAGGA AAACCTATAT CCTTATTTAG  1560
177  GCCCCAGCAC ACTCAGAGAC AGACCTCAGG ATATCATTGT GTTTGTAATT GGAGGAGCCA  1620
178  CCTATGAAGA GGCTCTAACA GTTTATAACC TGAACCGCAC CACTCCTGGA GTGAGGATTG  1680
179  TCCTGGGAGG CACCACAGTG CACAACACGA AAAGTTTCCT AGAGGAAGTT CTGGCTTCTG  1740
180  GACTGCACAG CCGAAGCAAG GAGAGCTCTC AAGTCACATC AAGGTCAGCG AGCAGAAGAT  1800
181  GAAACGGTGG TTGGGGGAAG GGCACAGCTT CCTCTCTTGT CCCCACTACA GGTTTTCCCT  1860
182  ACTAAACAAA GGTGTTGGAG AGCAGCTTTG GGTTCTGTGC TGGTTGTTAG AACTCATCTC  1920
183  CAGGTAGCCC ACGGATACGT GGTTGGCACA GACACAAGAC TCCCAGAGTT GTCCTAACAA  1980
184  TAAGTCTGAG CCCATCTCAA CCCACTTTTC TCCGGTAGTC TTTATGTATC TGTTAGCACA  2040
185  ATCACTTCAG TTACTGATGA ATTTTGTTGG GATCTGACTT GGGGAAAGGG TTATCAGAGC  2100
186  CTAGAGGGGC TTAAAAAGTA ATCATTTGAT GTACATACCA CACTCCTTGG CTTCCTTTCT  2160
187  CTTCCCTTAA CCCTTTCTGC TTTTCATTAA CCACATTCCT GCACAACTCA TTTCTGAAAA  2220
188  CCTACCATGT TTCTTTACAG AGCCATCCAA AAATTTTTTG TCCCTACATA GCAATTTTCT  2280
189  GTGGCACTGA GAAACCATGT ATGACCACAA TAAAAATCCA TTTTGTGAAA GGAAAAAAAA  2340
190  AA                                                                 2342
```

192 (2) INFORMATION FOR SEQ ID NO: 3:
194   (i) SEQUENCE CHARACTERISTICS:
195   (A) LENGTH: 194 amino acids
196   (B) TYPE: amino acid
197   (C) STRANDEDNESS: single
198   (D) TOPOLOGY: linear
200   (vii) IMMEDIATE SOURCE:
201   (A) LIBRARY: 2056691
202   (B) CLONE: BEP1NOT01
204   (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

```
206  Met Lys Ile Trp Thr Ser Glu His Val Phe Asp His Pro Trp Glu Thr
207   1               5                  10                 15
208  Val Thr Thr Ala Ala Met Gln Lys Tyr Pro Asn Pro Met Asn Pro Ser
209              20              25                 30
210  Val Val Gly Val Asp Val Leu Asp Arg His Ile Asp Pro Ser Gly Lys
211          35              40                 45
212  Leu His Ser His Arg Leu Leu Ser Thr Glu Trp Gly Leu Pro Ser Ile
213      50              55                 60
214  Val Lys Ser Leu Ile Gly Ala Ala Arg Thr Lys Thr Tyr Val Gln Glu
215  65              70              75                      80
216  His Ser Val Val Asp Pro Val Glu Lys Thr Met Glu Leu Lys Ser Thr
217              85              90                      95
218  Asn Ile Ser Phe Thr Asn Met Val Ser Val Asp Glu Arg Leu Ile Tyr
219              100             105                     110
220  Lys Pro His Pro Gln Asp Pro Glu Lys Thr Val Leu Thr Gln Glu Ala
221          115             120                     125
222  Ile Ile Thr Val Lys Gly Val Ser Leu Ser Ser Tyr Leu Glu Gly Leu
223          130             135                     140
```

RAW SEQUENCE LISTING   DATE: 06/29/2001
PATENT APPLICATION: US/09/556,178   TIME: 11:07:41

Input Set : N:\Crf3\RULE60\09556178.txt
Output Set: N:\CRF3\06292001\I556178.raw

```
224  Met Ala Ser Thr Ile Ser Ser Asn Ala Ser Lys Gly Arg Glu Ala Met
225  145             150             155             160
226  Glu Trp Val Ile His Lys Leu Asn Ala Glu Ile Glu Glu Leu Thr Ala
227              165             170             175
228  Ser Ala Arg Gly Thr Ile Arg Thr Pro Met Ala Ala Ala Ala Phe Ala
229              180             185             190
230  Glu Lys
233  (2) INFORMATION FOR SEQ ID NO: 4:
235      (i) SEQUENCE CHARACTERISTICS:
236          (A) LENGTH: 836 base pairs
237          (B) TYPE: nucleic acid
238          (C) STRANDEDNESS: single
239          (D) TOPOLOGY: linear
241     (vii) IMMEDIATE SOURCE:
242          (A) LIBRARY: 2056691
243          (B) CLONE: BEP1NOT01
245      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:
247  GAGCGGGGCA GGGGCAGGTG TAGCCTCTGT GCCTCGTTGT CCCCTGGCGC TACCCGGACA    60
248  TCTCTCAGGG TGCCGGCACC ATGAAGATCT GGACTTCGGA GCACGTCTTT GACCACCCGT   120
249  GGGAAACTGT TACAACAGCT GCAATGCAGA AATACCCAAA CCCTATGAAC CCAAGTGTGG   180
250  TTGGAGTTGA TGTGTTGGAC AGACATATAG ATCCCTCTGG AAAGTTGCAC AGCCACAGAC   240
251  TTCTCAGCAC AGAGTGGGGA CTGCCTTCCA TTGTGAAGTC TCTTATTGGT GCAGCAAGAA   300
252  CGAAAACATA TGTGCAAGAA CATTCTGTAG TTGATCCTGT AGAGAAAACA ATGGAACTTA   360
253  AATCTACTAA TATTTCATTT ACAAACATGG TTTCAGTAGA TGAGAGACTT ATATACAAAC   420
254  CACATCCTCA GGATCCAGAA AAAACTGTTT TGACACAAGA AGCCATAATT ACCGTGAAAG   480
255  GAGTTAGCCT CAGCAGTTAC CTTGAAGGAC TGATGGCAAG TACGATATCC TCAAATGCTA   540
256  GTAAAGGCCG AGAAGCAATG GAATGGGTAA TACATAAATT AAATGCTGAG ATTGAAGAAC   600
257  TGACAGCCTC AGCAAGAGGA ACCATAAGGA CTCCAATGGC AGCAGCAGCG TTTGCAGAGA   660
258  AGTGATCGTG ACAGTTGGTA GACAACATCG GGTACTCCAG GTCTCTCCAA ACTGACTATA   720
259  TATTTATTTG TTATTTTAAA AATACAACTA TATTTTGGGT AGTTTTTTTT TTTTTTTTTT   780
260  TTGATAAGTT GGTGTAAGGC TATGTGACTG ATCAAAACAG ATGCAGGGCC TCTAAA       836
262  (2) INFORMATION FOR SEQ ID NO: 5:
264      (i) SEQUENCE CHARACTERISTICS:
265          (A) LENGTH: 177 amino acids
266          (B) TYPE: amino acid
267          (C) STRANDEDNESS: single
268          (D) TOPOLOGY: linear
270     (vii) IMMEDIATE SOURCE:
271          (A) LIBRARY: HEAONOT03
272          (B) CLONE: 3086794
274      (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:
276  Met Glu Ala Leu Ile Leu Glu Pro Ser Leu Tyr Thr Val Lys Ala Ile
277   1           5               10              15
278  Leu Ile Leu Asp Asn Asp Gly Asp Arg Leu Phe Ala Lys Tyr Tyr Asp
279              20              25              30
280  Asp Thr Tyr Pro Ser Val Lys Glu Gln Lys Ala Phe Glu Lys Asn Ile
281          35              40              45
282  Phe Asn Lys Thr His Arg Thr Asp Ser Glu Ile Ala Leu Leu Glu Gly
283      50              55              60
```

VERIFICATION SUMMARY

DATE: 06/29/2001

PATENT APPLICATION: US/09/556,178

TIME: 11:07:42

Input Set : **N:\Crf3\RULE60\09556178.txt**
Output Set: **N:\CRF3\06292001\I556178.raw**

L:3 M:220 C: Keyword misspelled or invalid format, [(1) GENERAL INFORMATION:]
L:11 M:220 C: Keyword misspelled or invalid format, [(ii) TITLE OF INVENTION:]
L:30 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]
L:31 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]